

See ID NO: 1

TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 26 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..243
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 15; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAATGTTGCTCT 15
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Db 141 TTTAATGTTGCTCT 127

RESULT 2
AR083113/c 248 bp DNA linear PAT 01-SEP-2000
LOCUS AR083113
DEFINITION Sequence 27 from patent US 5976803.
ACCESSION AR083113
VERSION AR083113.1 GI:10009903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 248)
AUTHORS Week K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 27 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..248
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 15; DB 6; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAATGTTGCTCT 15
|||||
Db 146 TTTAATGTTGCTCT 132

RESULT 3
HUMADH7CIV 539 bp DNA linear PRI 07-MAR-1996
LOCUS HUMADH7CIV
DEFINITION Homo sapiens class IV alcohol dehydrogenase 7 (ADH7) gene, 5' flanking region.
ACCESSION L39009
VERSION L39009.1 GI:625123
KEYWORDS ADH7 gene; alcohol dehydrogenase; alcohol dehydrogenase IV.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 539)
AUTHORS Yokoyama, H., Barasona, E. and Lieber, C.S.
TITLE Upstream structure of human ADH7 gene and the organ distribution of its expression
JOURNAL Biochem. Biophys. Res. Commun. 216 (1), 216-222 (1995)
PUBMED 7488092
COMMENT Original source text: Homo sapiens DNA.
FEATURES Location/Qualifiers
source 1..539
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4q23-24"
/cell_type="fibroblast"
/tissue_type="foreskin"
/complement(1..539)
/gene="ADH7"
1..>539
/note="G00-362-911"
1..539
/note="G00-362-911"

ORIGIN
Query Match 100.0%; Score 15; DB 8; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAATGTTGCTCT 15
|||||
Db 338 TTTAATGTTGCTCT 352

RESULT 4
BV274862/c 638 bp DNA linear STS 25-JAN-2005
LOCUS BV274862
DEFINITION S232P6460RD5.T0 Beagle Canis familiaris STS genomic sequence tagged site.
ACCESSION BV274862
VERSION BV274862.1 GI:57437091
KEYWORDS STS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 638)
AUTHORS Lindblad-Toh, K.
TITLE The genome sequence of Canis familiaris
JOURNAL Unpublished (2004)
COMMENT Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477

SEQ ID NO: 3

misc_feature 488..496
/note="poc. glycosylation site"
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intron 542..1442
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repeat_region 882..1069
/note="Alu repetitive sequence"
exon 1443..1535
/number=5
intron 1536..1788
/number=5
exon 1789..1879
/number=6
intron 1880..2736
/number=6
exon 2737..2928
/note="additional exon 6B (used in 1441, omitted in 1431)"
repeat_region 2796..2928
/note="sequence homologous to the repetitive element in
thyroglobulin (Tyr)"
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/note="poc. glycosylation site"
misc_feature 2919..2927
/note="poc. glycosylation site"
intron 2929..3302
/note="6b"
exon 3303..3365
/number=7
intron 3366..3594
/note="intron VII"
exon 3595..4113
/number=8
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/note="putative"
ORIGIN
Query Match 100.0%; Score 14; DB 9; Length 4113;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATAGGCGAGAT 14
Db 1395 AAATAGGCGAGAT 1382

RESULT 28
SSU30500 4402 bp mRNA linear VRL 01-SEP-1995
LOCUS
DEFINITION sicilian sandfly fever virus glycoprotein precursor polypeptide
DEFINITION mRNA, complete cds.
ACCESSION U30500
VERSION U30500.1 GI:973314
KEYWORDS Sandfly fever sicilian virus
SOURCE Sandfly fever sicilian virus
ORGANISM Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus;

unclassified Phlebovirus.
REFERENCE 1 (bases 1 to 4402)
AUTHORS Glass, P.J. and Parker, M.D.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1995) Pamela J. Glass, Virology, USAMRIID, Bldg
1425, Ft. Detrick, Frederick, MD 21702, USA
FEATURES
source
1..4402
/organism="Sandfly fever sicilian virus"
/mol_type="mRNA"
/db_xref="taxon:28292"
19..404
/codon_start=1
/product="glycoprotein precursor polypeptide"
/protein_id="AA75043.1"
/db_xref="GI:973315"
/translation="MFEITILLIVLATFLVGNLSEKMGNSLSTCPSTGPG
IIEKNGFEAKMPGPDHCHRPBEGDFKRTHERNAKQIKYTTAPPTAKFGCDGT
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RTKEMEEVAVLDSNQIAHHEIQKENEIQKNDLRDAIKQGEHESKLRVES
DARVGLKEELKQLYKIFDHOATKDELQHAKEWQSLRKIKDPESIPQAKSSNS
VLTMTTAVLSLSSMAAPAGMNAATHINNRGLGKFPALITGTEDHCKKIDYGV
TCSRPHLKSIDRPFPNSHHRALLEHNDNIYKISSTISCTRTKRAECSKIR
KLAIKCRGVSVITADSGRTGELYCKENESLMEKCIQCRKVRKPKQGLIQLQD
MWCQNSTDYTGPKQVLKGYCKIGMDYRHCHEFASMEVVPFALFKKGLYMDSR
IRNKDVLEKENFICYKAGKENDADSSNHCQKSVYTECKNDVPSQNKICSGNTPCS
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GHLSHDEVQVSHRHHCEPKDCVVAHSCVCAEGILINQCHTLAFAVTVLVIA
VLMPLIVLAKCLAFRVAAILVLPFSWLVKLATSRKLSITERIARINSEICMR
PEGAAHARRDRDRIPRSAYVLAIIILSVTSACSDHTIASKIKYICVAKGSGV
CTISGLINVAAGPIGSECTVTLKGPDSADKKRTIKTIIASELICEGQSVQCYVE
CISPRRCVAGCECKDCAQRNNTVUSREFOITNNSVISENRCIEQCGVQGCACNV
YASCLFPAHRLAIRKRAIKVFNCIDWSHRLVLEITDFNCKEKVSMGTQTPFSWG
SMTLADPEIGITGNTSYSFLSSSGTFLSLVDLASMERPRGFLGSIKSSSAAALTAH
KSCVAPDIIRYKPMTDIVDCSTSLIDPFAVFLGALPQTRNGKTFSSSIDKTIQAF
TSGIVHASMISLSPNPEVEFEERVCLASPVNITGCGSCNBEARVCIOAANKVMTL
HYHTLDNSLTIIVDVLSPKSTDRVHLSLTPVMDVYVSCGYKAMSIAGLVAMN
PDDRHRHEETNSVYVNPRTGRMDSSNASGLVDMGLCPRLTAGVILGTITLAIIVPLIM
LVLCVPLVGMIRPALIKKKL"
ORIGIN
Query Match 100.0%; Score 14; DB 13; Length 4402;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAATAGGCGAGAT 14
Db 4168 AAATAGGCGAGAT 4181

RESULT 29
HSM807414/c 4703 bp mRNA linear PRI 30-AUG-2003
LOCUS
DEFINITION Homo sapiens mRNA; cDNA DKFZp686f2193 (from clone DKFZp686f2193).
ACCESSION BX647270
VERSION BX647270.1 GI:34366298

Seq ID NO: 4

Db 24 TCTTTGAGCACAGAT 38

RESULT 3

AA080645

LOCUS AA080645 266 bp mRNA linear EST 28-OCT-1997

DEFINITION EST100 Sugarcane leaf roll Saccharum sp. cDNA clone B80-rev similar to coded for by C. elegans cDNA, mRNA sequence.

ACCESSION AA080645

VERSION AA080645.1 GI:1620362

KEYWORDS EST.

SOURCE Saccharum sp.

ORGANISM Saccharum sp.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE 1 (bases 1 to 266)

AUTHORS Carson, D.L. and Botha, F.C. \subseteq

TITLE Sugarcane cDNA from leaf roll tissue

JOURNAL Unpublished (1996)

COMMENT Contact: Deborah Lee Carson

Biotechnology

South African Sugar Association Experiment Station

Private Bag X02, Mount Edgecombe, 4300, South Africa

Tel: 2731593205

Fax: 2731595406

Email: biotech@sugar.org.za

Partial sequence of a 500 bp clone

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..266

/organism="Saccharum sp." \subseteq

/mol_type="mRNA"

/db_xref="taxon:15819"

/clone="B80-rev" \subseteq

/tissue_type="leaf roll"

/clone_lib="Sugarcane leaf roll"

/note="Vector: Lambda ZAP II; Site_1: EcoRI; mRNA was prepared from the leaf roll of the commercial sugarcane variety Nco 376. cDNA was synthesised using standard protocols and ligated to an annealed amplification adaptor set. cDNA was then PCR amplified. Amplified cDNA was ligated and cloned into the Eco RI site of the Lambda ZAP II phage vector." \subseteq

ORIGIN

Query Match 100.0%; Score 15; DB 1; Length 266;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTTTGAGCACAGAT 15

|||||

Db 106 TCTTTGAGCACAGAT 120

RESULT 4

DN955667/c

2

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LAGAGAKTRFGSPNCYARHLHPRTPTPTQPSPLASHLTFNLNDADWMVSPVN
YEDRDQKFSQRRHYKEFRDLTQIPGHEANTVAEPRIYDKGNHRFENETIKLSIYQ
IKIETYNRADILFLDTRTKQALDVGDFDITVSNHNVINQNNLGLQCAETDQ
NSINVASGLVGRHGQSPKQFWFAFSEKVELLRVAAASKRKNKNKNSHODPS
KMPSPKQVNTSQEQAKCKHELHYFSDRLGHQMDIITAPESQAFYCDGEGSFPLNAHM
NANTHAIYVQTLVLHMFDPHPKPCCAPTKLNAISVLYFDSSNVILKKLYRNVVRSCG

ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 1359;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels

1 GGAGAGCAGTGAC 14
|||||
562 GGAGAGCAGTGAC 575

Accession	LOCUS	Size	Source	Accession
BC061764	<i>Rattus norvegicus</i>	1413 bp	mRNA	linear
IMAGE:5621087	<i>Rattus norvegicus</i>	partial cds.	protein kinase inhibitor p58	mRNA (cDNA clone)

DE0001704
 ACCESSION BC061764.1 GI:38197557
 KEYWORDS .
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

1 (bases 1 to 1413)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zierberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, N.J., Usdin, T.B., Toshiyuki, S., Carncini, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, D.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E.,
Schermer, A., Schein, J.E., Jones, S.J. and Warra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL
PUBMED

Seq ID NO:6

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/db_xref="taxon:7242"

ORIGIN
Query Match 100.0%; Score 14; DB 6; Length 2963;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATTGTCCTATG 14
|||||
Db 855 ACATTGTCCTATG 842

RESULT 19
XLU17249 3562 bp mRNA linear VRT 27-SEP-1995
LOCUS
DEFINITION Xenopus laevis gastric H(+) -K(+) -ATPase alpha-subunit mRNA,
complete cds.
ACCESSION U17249
VERSION U17249.1 GI:596055
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE
AUTHORS Mathews,P.M., Claeys,D., Jaisser,F., Geering,K., Horisberger,J.D.,
Kraehenbuhl,J.P. and Rossier,B.C.
TITLE Primary structure and functional expression of the mouse and frog
alpha-subunit of the gastric H(+) -K(+) -ATPase
JOURNAL Am. J. Physiol. 268 (5 Pt 1), C1207-C1214 (1995)
PUBMED 7762614
REFERENCE 2 (bases 1 to 3562)
AUTHORS Mathews,P.M.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1994) Paul M. Mathews, Institute of Pharmacology
and Toxicology, University of Lausanne, Rue du Bugnon 27, CH-1005,
Lausanne, Switzerland
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/sex="female"
/cell_type="parietal cell"
/tissue_type="stomach mucosa"
/dev_stage="adult"
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/db_xref="GI:596056"
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STNIIASFNLVPOQATVVRDGDQFIINQLVVGDLVEIKGDRVPADIRIITSQGC
KVNSSSLTGESEPQTRSPETHESPLETRNIAFFSTMCLEGTATGTLIINTGDRTIIGR
IATLASGVGNEKTPIAIEIHFDVDDIAGLAIFGGAFFVAVMVGITFLRAMVFMNAI
VVAVYFEGLLATVTVCLSLTAKRLAKNCVKNLEAVEITLGSTVISCDSKGTGLTONR
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KLYMVGAPERILERCSTINIKQQLPLDEQKEAFQATYMDLGLGIGSERVIGFCHLY
LNEKEYRGFNFTDEEMFTSGCLCFAGLISMIDPPRATVPDAVMKCTAGIRIVMT
GDHPITAKIAASVGIISSESTVEDIAARLRIPEQVNRKARACVINGQKEMSS
BELVEALKLHPMEVFARTSPQOKLIIVESCQKLAGI VAVTGQVNDSPALKKADICVA
MGISDAAKNAADMILLDDNFASIVTVEQGLIFDNLKKSIAVTLTKNIPELAPYL
IYITASVPLPGCTITLIELCTDIPEVSILAYERAESDMLHLKPNRDRDLVNEAL
AVYSYFQIGIIQSAGFVDVYFTVMAQEGMFFAYIGLRSWHENQHLQDLQDSYQGBWT
FSQRLYYQYTCYTVFFIISYEICQISDLVLRKLSVFOQGFGRKVLAIIVFQLCL
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Y"
polya_site 3562
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Query Match 100.0%; Score 14; DB 5; Length 3562;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATTGTCCTATG 14
|||||
Db 3210 ACATTGTCCTATG 3223

RESULT 20
AC006119/1
LOCUS AC006119 5207 bp DNA linear ROD 04-DEC-1998
DEFINITION Mus musculus clone UMGC:mbac10gap from 14D1-D2 (T-Cell Receptor
Alpha Locus), complete sequence.
ACCESSION AC006119
VERSION AC006119.1 GI:3962517
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 5207)
Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,
Magness,C.L., Green,P., Olson,M.V. and Hood,L.
TITLE Large-Scale Sequence Analysis of the Mouse T-Cell Receptor Alpha
Locus
JOURNAL Unpublished (1998)
REMARK University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Inyoud Lee (borah@u.washington.edu)
2 (bases 1 to 5207)
Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,
Magness,C.L., Green,P., Olson,M.V. and Hood,L.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
COMMENT
Overlapping Sequences:
5': UMGC:mbac37 (Genbank Accession: AC005402)
3': UMGC:mbac92 (Genbank Accession: AC005855)
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Seq ID NO: 7

JOURNAL COMMENT
Unpublished (2005)
Contact: William Gregory
Nematode Genomics, University of Edinburgh
ICAPB
Ashworth Laboratories, King's Buildings, Edinburgh, EH9 3JT
Tel: +44 131 650 7317
Email: b.gregory@ed.ac.uk
The library was constructed in pSPORT1 vector (Invitrogen) using
Generacer (Invitrogen) 5' capped adult female mRNA by William
Gregory, University of Edinburgh. Sequencing was performed by PSU,
Sanger Centre, Cambridge, UK.
Plate: 19 row: e column: 01
Seq primer: T7(TAATACGACTCACTATAGG)
High quality sequence stop: 241.

FEATURES

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1..282
Location/Qualifiers
/organism="Litomosoides sigmodontis"
/mol_type="mRNA"
/db_xref="taxon:42156"
/clone="Ls afl_19e01"
/sex="Female"
/clone_lib="Litomosoides sigmodontis adult female 1 (high
molecular weight)"

ORIGIN

Query Match 100.0%; Score 15; DB 8; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATCTAGATCAATT 15
|||||
Db 217 GCATCTAGATCAATT 203

RESULT 3
AA906249
LOCUS AA906249 385 bp mRNA linear EST 19-MAY-1998
DEFINITION oJ93g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1505926 3' similar to contains L1.t3 L1 repetitive element ;
mRNA sequence.
ACCESSION AA906249
VERSION AA906249.1 GI:3041372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 385)
AUTHORS NCIC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@email.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 830 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 367.

FEATURES

source
1..385
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1505926"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-CCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 15; DB 1; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATCTAGATCAATT 15
|||||
Db 266 GCATCTAGATCAATT 280

RESULT 4
B83992/c
LOCUS B83992 400 bp DNA linear GSS 09-APR-1999
DEFINITION RPC111-21H8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-21H8,
genomic survey sequence.
ACCESSION B83992
VERSION B83992.1 GI:2925124
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPC111-21H8.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research